

FIG. 1

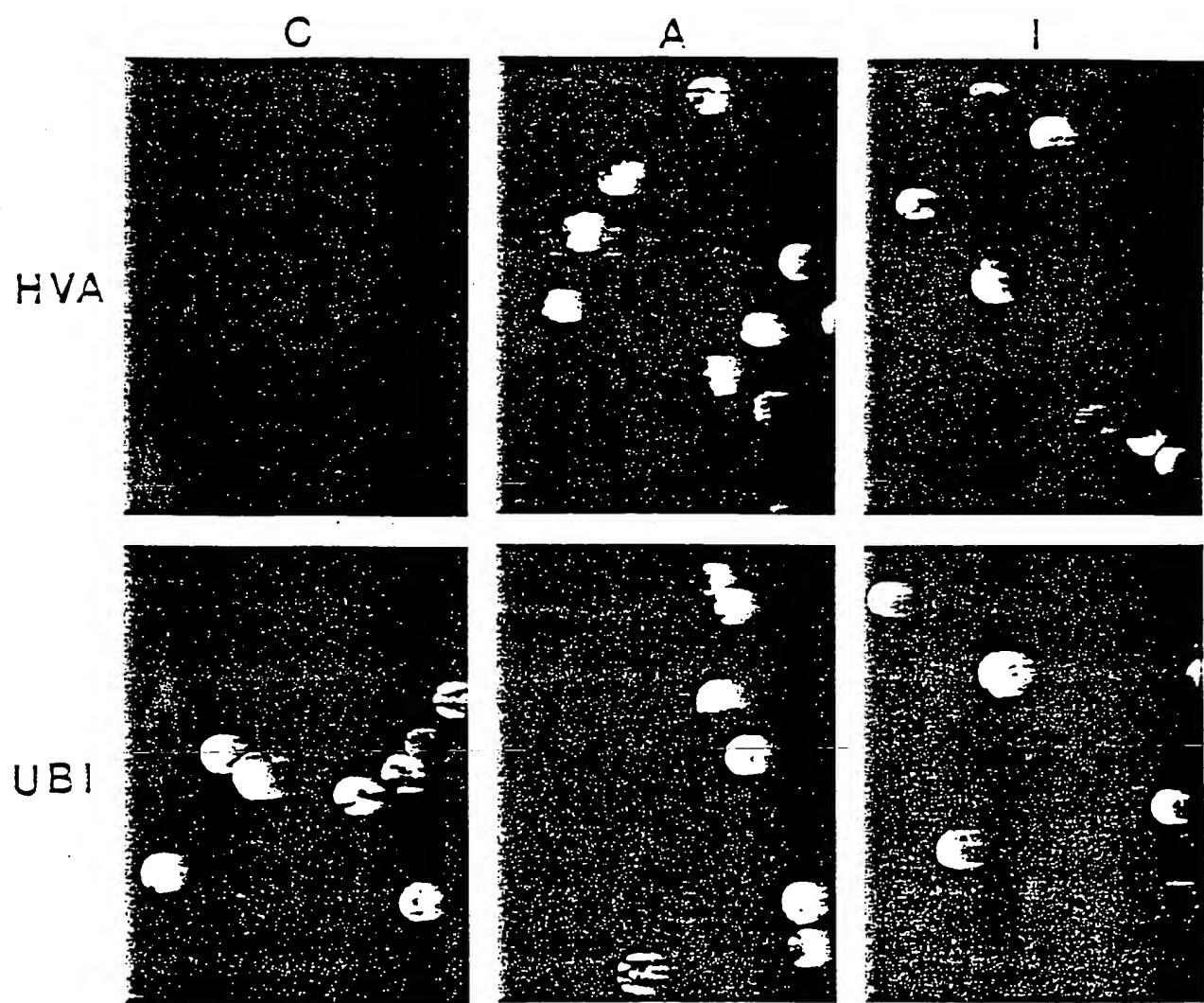


FIG. 2

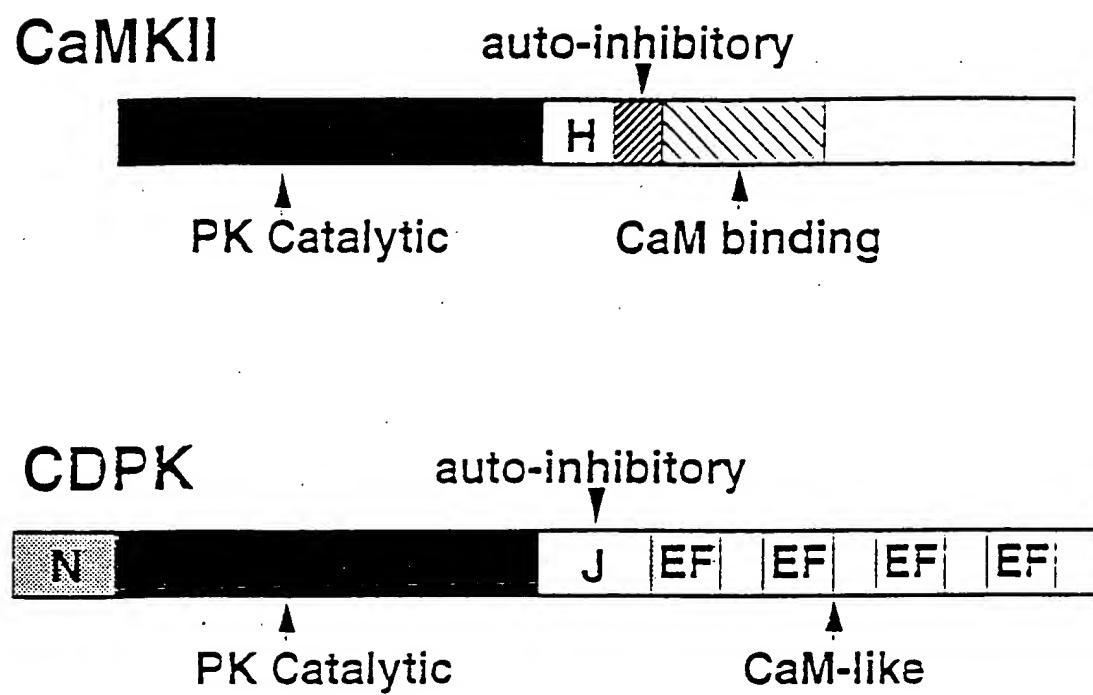


FIG. 3A

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FIG. 3B

## PK Constructs

	1 a.a. ATG	413 a.a.	TGA
1.	<b>35SC4PPDK</b>	ATCDPK (AK1)	DHA NOS
2.	<b>35SC4PPDK</b>	ATCDPK1	274 a.a. DHA NOS
3.	<b>35SC4PPDK</b>	ATCDPK1a	274 a.a. DHA NOS
4.	<b>35SC4PPDK</b>	ATCDPK2	289 a.a. DHA NOS
5.	<b>35SC4PPDK</b>	ATPKa	284 a.a. DHA NOS
6.	<b>35SC4PPDK</b>	ATPKb	283 a.a. DHA NOS
7.	<b>35SC4PPDK</b>	ASK1	265 a.a. DHA NOS
8.	<b>35SC4PPDK</b>	ASK2	265 a.a. DHA NOS

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d

0 1 2 3 4 5 6 7 8 M

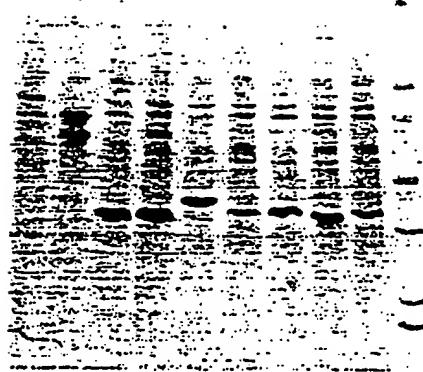


FIG. 3D

✓ GATTCTTCTGGG

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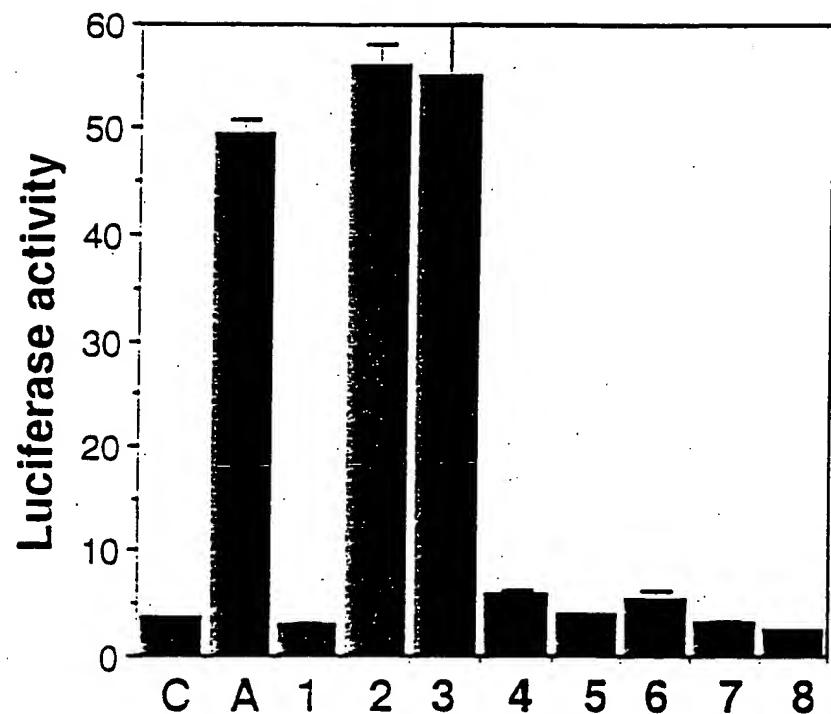


FIG. 3E



FIG. 4A

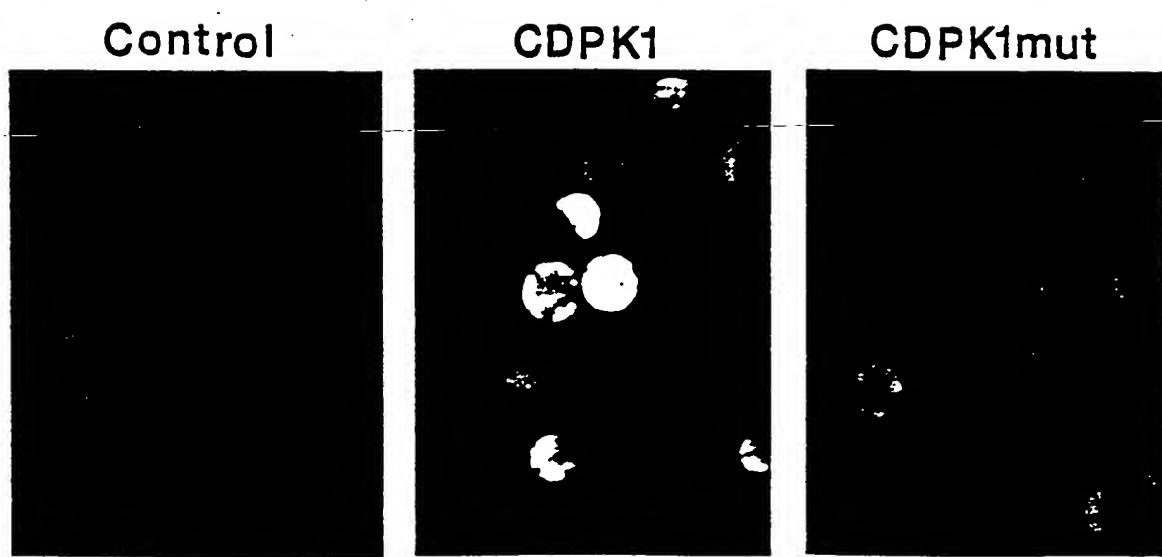


FIG. 4B

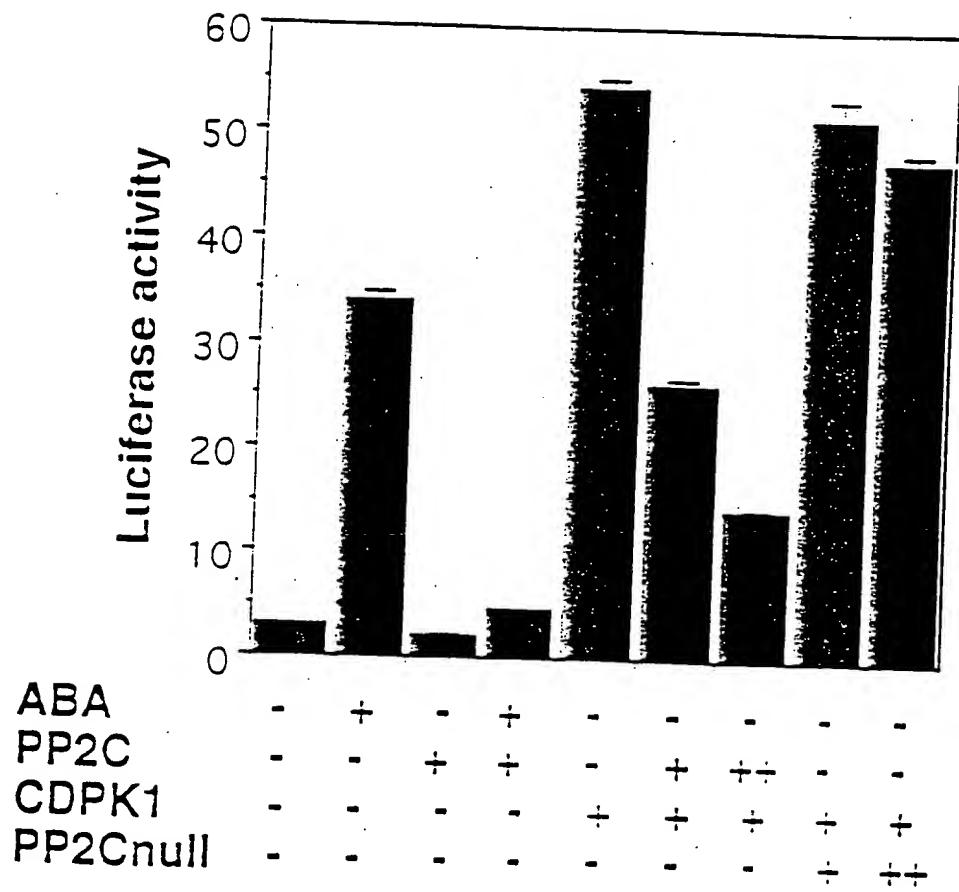


FIG. 4C

## A model of stress signalling in plant cells

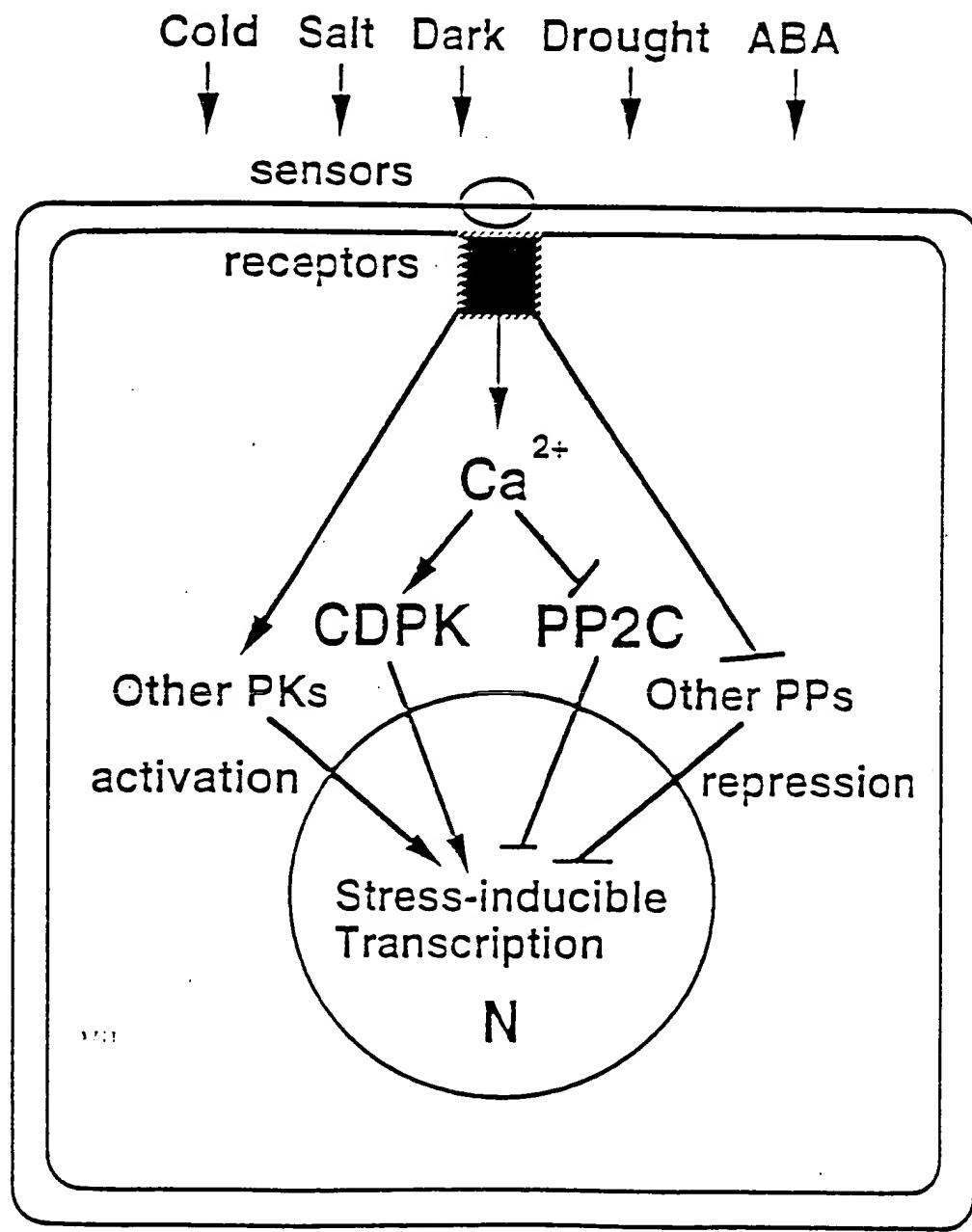


FIG. 4D

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FIGURE 5 (SHEET 1/4)

SEQ ID NO: 1 →  
1 GTTGTAAACGACGGNCAGTCATTGTAATACGACTCNCTATAGGGCGNAATTGGAGCTC  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
CAACATTTTGCTGCCNGTCACTTAACATTATGCTGAGNGATATCCCGCTAACCTCGAG

a

61 CACCGCGGTGGCGGCCGCTCTAGAAGCTAGTGGATCCATGGCTAACAACTCAGATCAGC  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
GTGGCGCCACCGCCCGCGAGATCTTGATCACCTAGGTACCCATTAGTTTGAGTCTAGTCG

SEQ ID NO: 2 → M A N Q T Q I S -

121 GACAAGTACATCTTAGGACGGAGAACTCGTCGGCGAATTCCAATCAGTATCTTGT  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
CTGTTCATGTAGAATCCTGCTCTTGAGCCAGCGCCGCTTAAGCCTTAGTGCATAGAACAA

a ~ D K Y I L G R E L G R G E F G I T Y L C -

FIGURE 5 (SHEET 2/4)

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ACAGATAGAGAGACTCGTGAAGCTTTAGCTTCAAATCAATCTCAAGAGAAAGCTCCGA 240
181 -----+-----+-----+-----+
TGTCTATCTCTGAGCCTTCGAAATCGAACGTTAGTTAGAGGTTCTCTTCGAGGCT

. T D R E T R E A L A C K S I S K R K L R -
```

```

ACCGCCCTCGATGTGAAAGACGTCCGTGAAAGTCACGATCATGTCACCTTACCGGAA 300
241 -----+-----+-----+-----+
TGGCGGCAGCTACACCTTCTGCAGGCAGCAGTCAGTGCTAGTACAGTTGAAATGGCCTT

. T A V D V E D V R R E V T I M S T L P E -
```

```

CACCCAACGTTGTGAAACTTAAGCGACTTATGAGGATAACGAGACCGTGCATCTTGTG 360
301 -----+-----+-----+-----+
GTGGGTTTGCACACTTGTGAAATTGCTGAATACTCTTATGCTCTGGCACCTAGAACAC

. H P N V V K L K A T Y E D N E T V H L V -
```

```

ATGGAGCTTGAGGAGGTGAGCTTTGGTCGGATTGTTGCAAGAGGACATTATACA 420
361 -----+-----+-----+-----+
TACCTCGAAACACTCCCTCACTCGAAAACCAGCCTAACACGTTCTCTGTAAATATGT

. M E L C E G G E L F G R I V A R G H Y T -
```

17.1

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GAGCGTGGCGGGCGCTACCGTCGGAGAACGATCGCCGAGTTGTGAGGATGTGTATGTC 480
421 -----+-----+-----+-----+
CTCGCACGCCGCCATGGCAGCGCTTGTAGGCCCTTCAACACTCTACACAGTACAG

. E R A A A T V A R T I A E V V R M C H V -
```

FIGURE 5 (SHEET 3/4)

D E C E M B E R 1 9 9 4

481 AATGGTGTATGCATAGAGATTGAAAGCCTGAGAATTCTTGTGCTAACAGAAGGAG 540  
 TTACCAACAATACGTTATCTCTAAACTTCGGACTCTTAACAAACAAACGATTGTTCTTCCTC  
 a N G V M H R D L K P E N F L F A N K K E -

541 // AATTCTGCACTRAGGCTATTGATTGGTTATCTGTTCTCTAAACCTGGAGAGAGG 600  
 TTAAGACGTGAATTCCGATAACTAAACCAAATAGACAAGAGAAATTGGACCTCTCTCC  
 a N S A L K A I D F G L S V L F K P G E R -

601 TTTACAGAGATTTGGAAGTCCTTATTATGGCTCCAGAAGTGTGAAAGAAATTAT 660  
 AAATGTCTCTAACACCTTCAGGAATAATACCGAGGTCTCACAACTCTCTTATA  
 a F T E I V G S P Y Y M A P E V L K R N Y -

661 GGACCAGACGGTTCATGTGTGGAGTCTGGAGTTATCCTCTACATCTTGCTTGTTGTT 720  
 CCTGGTCTCCAACCTACACACCTCACGACCTCAATAGGAGATGTAGAACGAAACACCAA  
 a G P E V D V W S A G V I L Y I L L C G V -

FIGURE 5 (SHEET 4/4)

721 CCTCCGTTTGGCCAGAGACTGAACAGGTGTGGCTTGCCAT...TGAGGGAGTTCTT  
 GGAGGC~~AA~~ACCC~~CT~~TCTGACTTGTCCACACCGAGAACGGT~~AGA~~ACTCCC~~TC~~AAGAA  
 P P F W A E T E Q G V A L A I L R G V L -

781 GATTAAAGAGAGATCCTTGGTCGCAGATATCAGAGAGCGCAAAGAGCCTTGTGAAGCAG  
 CTAAAATTCTCTAGGAACCAGCGTCTATAGTCCTCGCGTTCTCGGAACACTTCCGTC  
 D F K R D P W S Q I S E S A K S L V K Q -

841 ATGTTGGAACCTGATTCAACTAACGCTTGA~~T~~ACTGCTCAGCAAGTTCTTGATCACCC~~TT~~GG  
 TACAACCTTGGACTAAGTTGATT~~CG~~AAACTGACGGAGTCGTTCAAGAA~~T~~ACTAGTGGGAACC  
 M L E P D S T K R L T A Q Q V L D H P W -

901 ATACAGAA~~T~~GCAAAGAA~~R~~GGATCAAC~~C~~TTATCGATA~~CC~~GTGAC~~C~~TGGACGGGGGGGGGG  
 TATGTCTTACGTTCTTCTAGTTCTAGCTATGGCAGCTGGAGCTCCCCGGGG  
 I Q N A K K

961 GGTACCA~~G~~CTTNGT~~T~~CC~~T~~TTAGTGAGGGTTAATT~~T~~CGAGCTTGGCGTAATCATGTCAT  
 CCATGGTCGAA~~AN~~CA~~GG~~AAATC~~A~~CTCCC~~A~~TTAAAGCTCGAACCCATTAGTACAGTA